Figure 1. (SEQ ID NO: 1)

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TATCCTGTGGTAATGAGTTAATGCATTTAGAAGCACATGGCAGAACTAGGAGATCTGTGG 540

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CTGAGGCTAGTTTCTTGAGCTGACTGTAAATTTTGTGAGAATATTTTCAAGACTACATTA 660

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GGG 723

Figure 2.

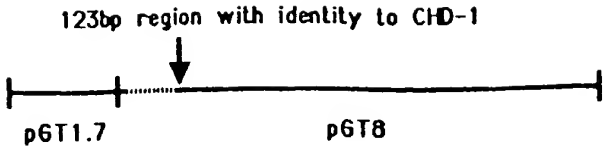

Figure 3.

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C  CHD-W    ATTTTACCTG ATGATCCAGA TAAGAAACCC CAGGCTAAGC AGTTACAGAC (SEQ ID NO: 4)
GT CHD-W    ATTTTACCTG ATGACCCAGA TAAGAAACCA CAGGCAAAGC AGTTGCAGAC (SEQ ID NO: 5)

M  CHD-1    CAAAAAACCA CAAGCAAAAC AGTTACAGAC CCGTGCAGAC TACCTCATCA
C  CHD-1A   CAAGAAACCC CAGGCAAAGC AGCTACAGAC CCGTGCAGAC TACCTCATTA
C  CHD-W    CAAGAAACCC CAGGCTAAGC AGTTACAGAC CCGTGCAGAT TACCTCATTA
GT CHD-W    CAAGAAACCA CAGGCAAAGC AGTTGCAGAC CCGTGCAGAT TACCTCATTA

M  CHD-1    AACTACTTAG CAGAGATCTT GCAAAAAGAG AGGCTCAGAG ACTTTGTGGT GCG
C  CHD-1A   AATTACTGAA TAAAGACCTT GCAAGAAAGG AAGCACAAAG GCTTGCTGGT GCA
C  CHD-W    AATTACTGAA TAAAGACCTT GCAAGAAAGG AAGCACAGAG ACTTGCTGGT GCA
GT CHD-W    AATTACTGAA TAAAGACCTT GCAAGAAAAG AAGTGCAAAG ACTTACTGGT GCA

M  CHD-1    ILPDDPDKKPQAKQLQTRADYLIKLLSRDLAKREAQRLCGA (SEQ ID NO: 6)
C  CHD-1A   ILPDDPDKKPQAKQLQTRADYLIKLLNKDLARKEAQRLAGA (SEQ ID NO: 7)
C  CHD-W    ILPDDPDKKPQAKQLQTRADYLIKLLNKDLARKEAQRLAGA (SEQ ID NO: 8)
GT CHD-W    ILPDDPDKKPQAKQLQTRADYLIKLLNKDLARKEVQRLTGA (SEQ ID NO: 9)
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Figure 5. (SEQ ID NO: 10)

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 151  GGAGTACCAG AAAGGGGATT CTTGACCTAC ACCTTGTAAC CTGAGTGGAC
 201  TTTCTTTTTA ACTTCTTAAT ACTTACAATG AATGGGCACA GTGATGAAGA
 251  AAGTGTAAGA AACAGCAGTG GAGAGTCAAG CAGATCAGAT GATGATTCTG
 301  GGTCAGCTTC AGGTTCTGGA TCTGGTTCAA GCTCTGGAAG CAGTAGCGAT
 351  GGAAGTAGCA GCCAGTCAGG TAGCAGTGAC TCTGAATCTG GTTCAGAGTC
 401  AGGCAGTCAA TCCGAATCAG AGTCTGACAC ATCTAGAGAG AAGAAACAAG
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 901  ATAAGAGAGG ATCTCGTCGC CAGGCAACAG TGAATGTTAG TTACAAAGAA
 951  GCTGAAGAAA CCAAGACAGA TTCTGATGAT TTGCTGGAAG TTTGTGGAGA
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1401  ATTGCTCATT CAAATCAAAA GTCAGCAGCT GGTTATCCGG ACTACTATTG
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3151  AAGAACCTGA AGGAGAAGAA CAGGAGCCCC AGGAAATGGA TATAGATGAA
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3301  ATGAAGATGA TATTGAGTTG GAACCAGAAA GAAATTCAAG AAATTGGGAA
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4351  TGAAATCTGA AAATAAAGAA AAATCTAAAA AAATTCCATT GCTGGATACT
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6251  TTTTTGGTTG TTTTATTTTA TTTTTTTTTT CTATTAAACT GTCAGTGTTG
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Figure 6.

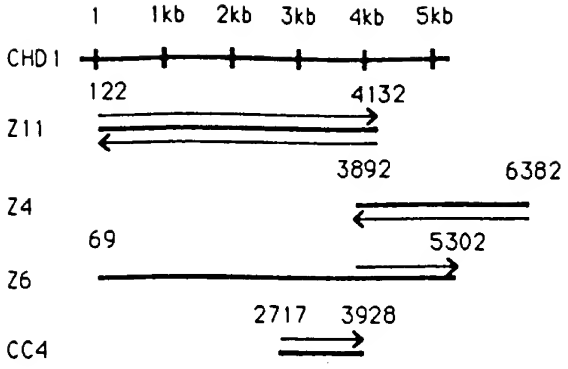

Figure 7.

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CHD-W      1  GATGGGATTGTTTCAGTGAAACATCCACATAAAAAAATAAAAGCAGAAA  (SEQ ID NO:  13)
                 D  G  I  V  S  V  K  H  P  H  K  K  I  K  A  E  (SEQ ID NO:  14)

                 K  E  N  E  E  K  P  E  P  D  I  G  I  K  K  E  A
CHD-1A    51  AAAGAAAAATGAAGAAAAGCCTGAGCCAGATATTGGTATAAAGAAGGAAGCT
CHD-W     51  AAAGAAAAATGAAGAAAAAGATGAGCCAGAGATTGGTATAAAGAAGGAAGCT
                 K  E  N  E  E  K  D  E  P  E  I  G  I  K  K  E  A

                 E  E  K  R  E  T  K  E  K  E  N  K  R  E  L  K  R
CHD-1A   101  GAAGAAAAAAAGAGAGACAAAAGAGAAGGAAAATAAAAAGGGAATTGAAAAGG
CHD-W    101  GCAGAAAAAAAGAGAGACAAAAGAGAAGGAAAATAAGA
                 G  E  K  R  E  T  K  E  K  E  N  K

                 E  K  K  E  K  E  D  K  K  E  L  K  E  K  D  N  K
CHD-1A   151  GAGAAAAAAGAAAAAGAGGATAAGAAAGAATTAAAAGAAAAAGATAATAAA

                 E  K  R  E  N  K  V  K  E  S  T  Q  K  E  K  E  V
CHD-1A   201  GAAAAGAGAGAAAACAAAGTAAAAGAATCCACACAGAAAGAAAAAGAAGTG

                 K  E  E  K
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10
in 137
93%07 D

Figure 8. (SEQ ID NO: 15)

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        90        100        110        120        130        140        150        160
AGGAAGAGTT ATCAGCAATT TTGAAGTTTG GTGCTGAGGA ACTTTTTAAA GAACCTGAAN NNGAAGAAGA GGAGCCTCAG
       170        180        190        200        210        220        230        240
GAGATGGATA TAGATGAAAT CCTGAAGAGG NCTGAAACTC GAGAAAATGA GTCAGGCCCA TTAACTGTAG GAGATGAGTT
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       490        500        510        520        530        540        550        560
TTCTGGATCT GATAGTGATT CCATCTCAGA AAGAAAACGA CCAAAAAAAC GTGGACGACC ACGAACTATT CCCCGTGAAA
       570        580        590        600        610        620        630        640
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GATGCTATAG CTAGAGATGC TGAGCTAGTT GATAAATCTG AAACAGACCT TAGACGTCTG GGAGAACTTG TACATAATGG
       730        740        750        760        770        780        790        800
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       810        820        830        840        850        860        870        880
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       890        900        910        920        930        940        950        960
CCTTCAGATC CAGAAGAAAG GAAAAGATAT GTCATCCCAT ACCACACCAA AGCAGCTCAT TTTGATATAG ATTGGGGTAA
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      1130       1140       1150       1160       1170       1180       1190       1200
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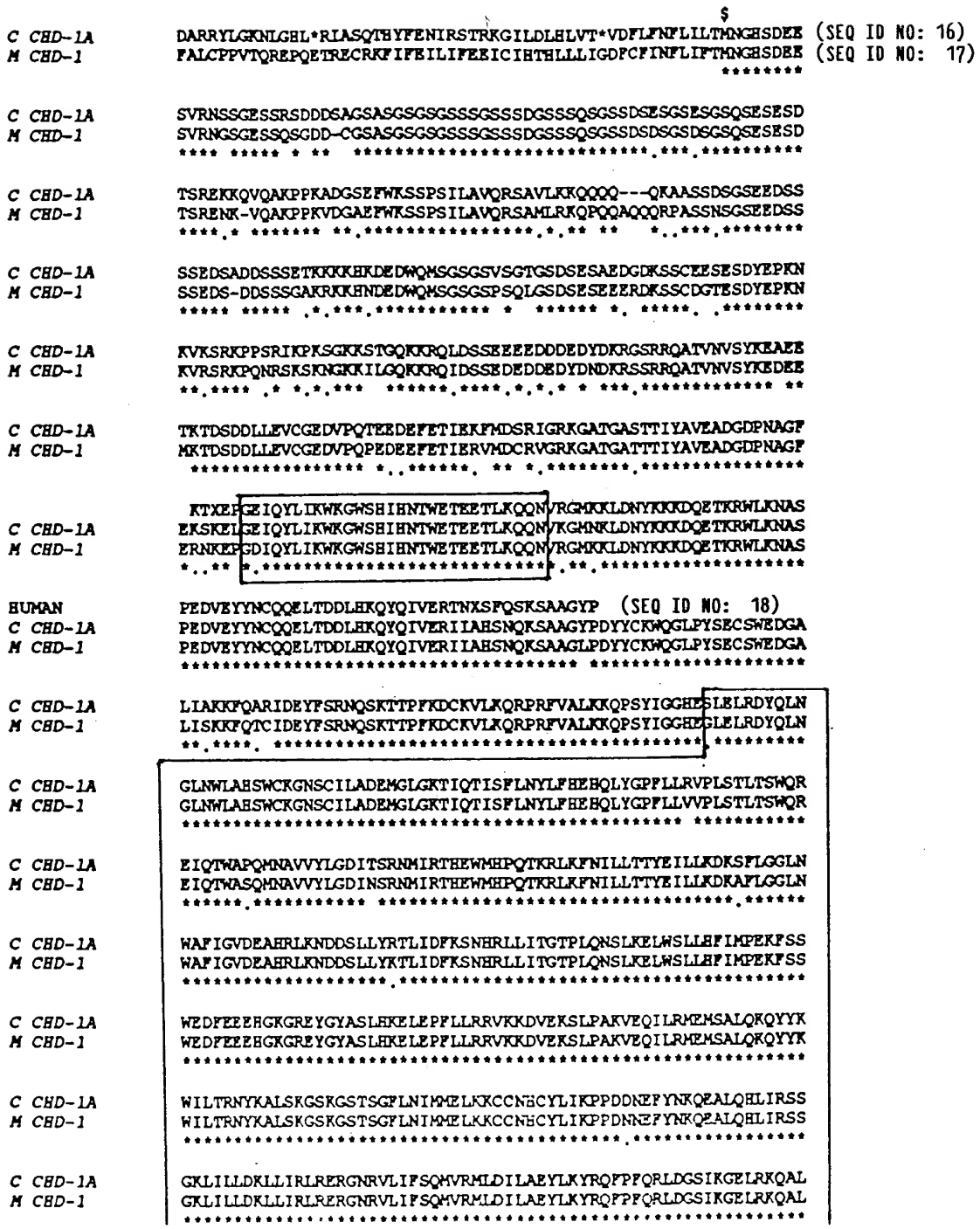
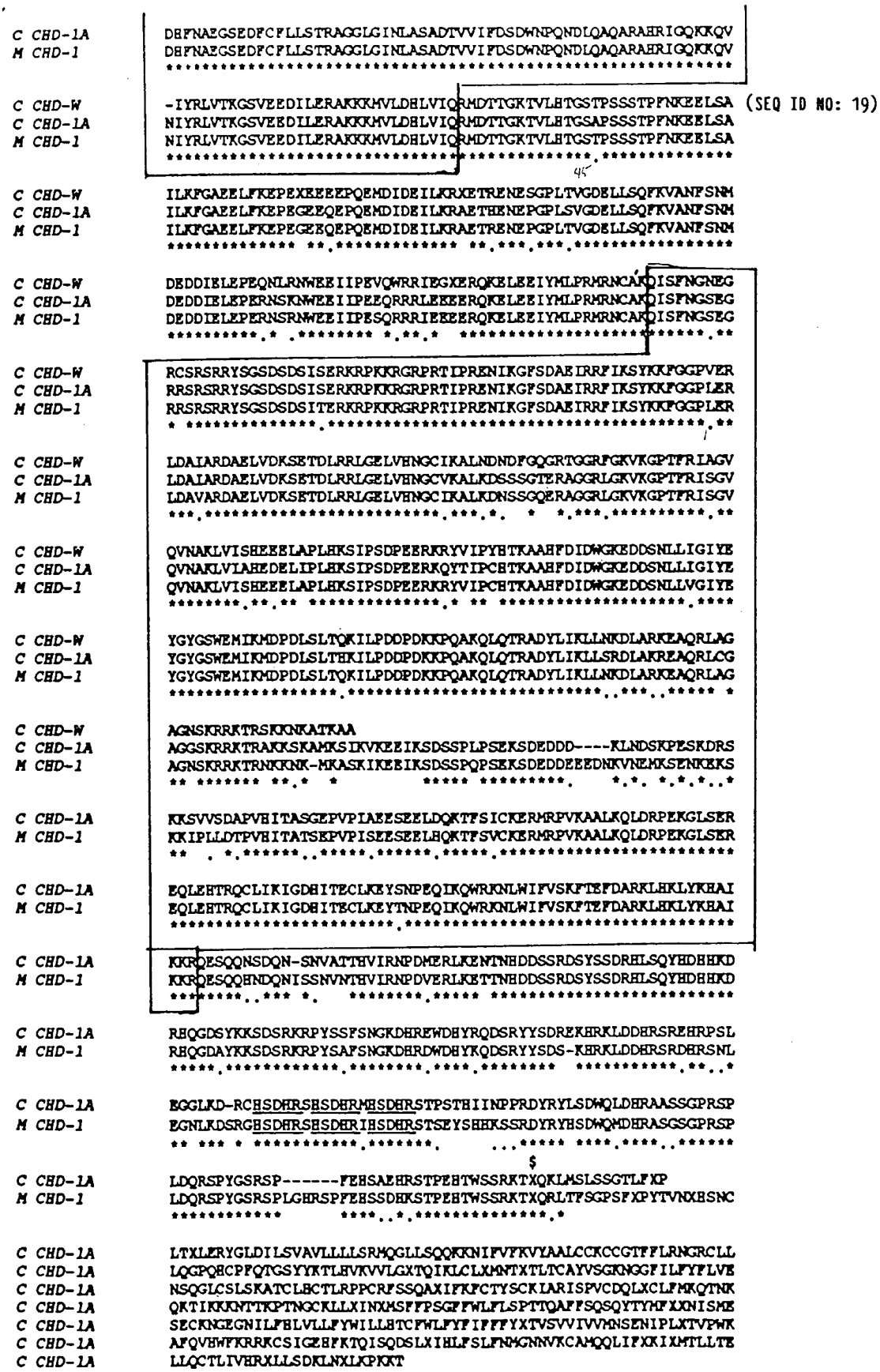
Figure 9.

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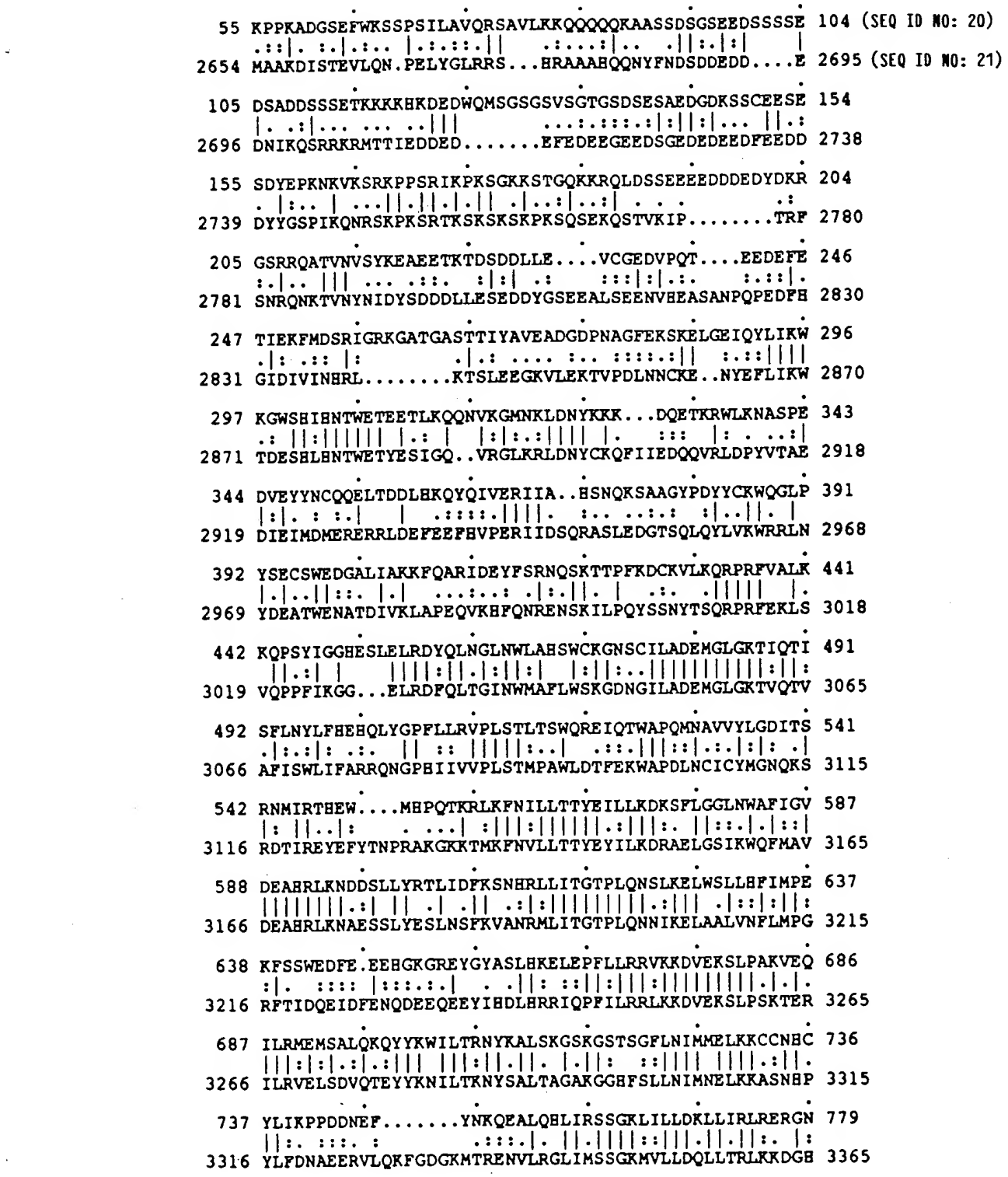
(SEQ ID NO: 19)

Figure 10.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542 RNMIRTHEW....MHPQTKRLKFNILLTTYEILLKDKSFLGGLNWAFIGV 587
3116 RDTIREYEFYTNPRAKGKKTMKFNVLLTTYEYILKDRAELGSIKWQFMAV 3165
588 DEAHRLKNDDSLLYRTLIDFKSNHRLLITGTPLQNSLKELWSLLHFIMPE 637
3166 DEAHRLKNAESSLYESLNSFKVANRMLITGTPLQNNIKELAALVNFLMPG 3215
638 KFSSWEDFE.EEHGKGREYGYASLHKELEPFLLRRVKKDVEKSLPAKVEQ 686
3216 RFTIDQEIDFENQDEEQEEYIHDLHRRIQPFILRRLKKDVEKSLPSKTER 3265
687 ILRMEMSALQKQYYKWILTRNYKALSKGSKGSTSGFLNIMMELKKCCNHC 736
3266 ILRVELSDVQTEYYKNILTKNYSALTAGAKGGHFSLLNIMNELKKASNHP 3315
737 YLIKPPDDNEF.....YNKQEALQHLIRSSGKLILLDKLLIRLRERGN 779
3316 YLFDNAEERVLQKFGDGKMTRENVLRGLIMSSGKMVLLDQLLTRLKKDGH 3365

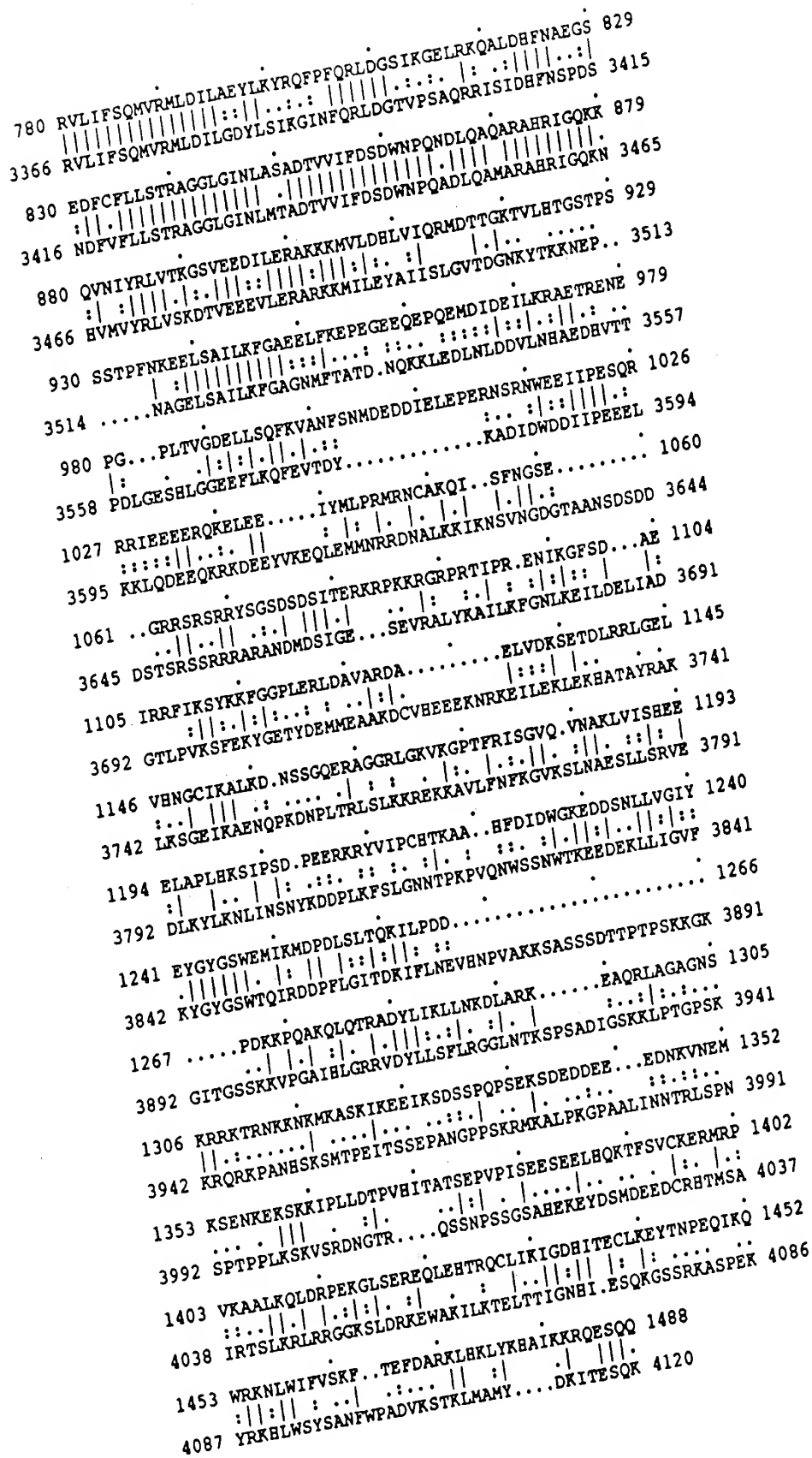

Figure 11.

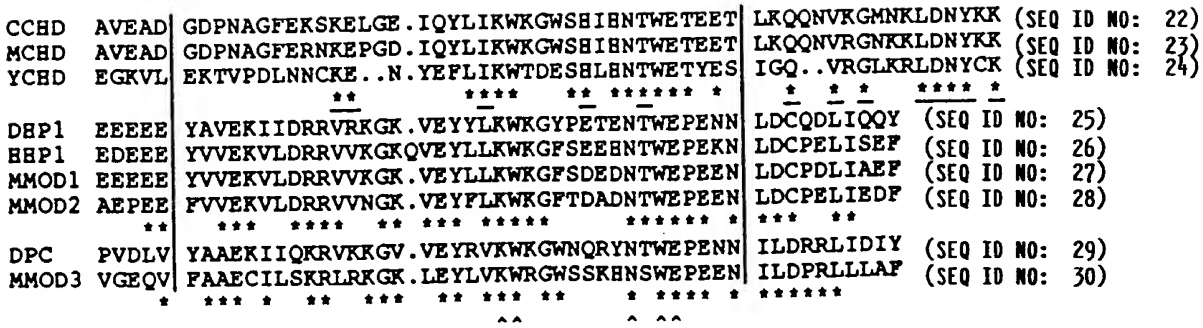
CCHD AVEAD GDPNAGFEKSKELGE.IQYLIKWKGWSHIHNTWETEET LKQQNVKGMNKLDNYKK (SEQ ID NO: 22)
MCHD AVEAD GDPNAGFERNKEPGD.IQYLIKWKGWSHIHNTWETEET LKQQNVRGNKKLDNYKK (SEQ ID NO: 23)
YCHD EGKVL EKTVPDLNNCKE..N.YEFLIKWTDESHLHNTWETYES IGQ..VRGLKRLDNYCK (SEQ ID NO: 24)
DHP1 EEEEE YAVEKIIDRRVRKGK.VEYYLKWKGYPETENTWEPENN LDCQDLIQQY (SEQ ID NO: 25)
HHP1 EDEEE YVVEKVLDRRVVKGKQVEYLLKWKGFSEEHNTWEPEKN LDCPELISEF (SEQ ID NO: 26)
MMOD1 EEEEE YVVEKVLDRRVVKGK.VEYLLKWKGFSDEDNTWEPEEN LDCPDLIAEF (SEQ ID NO: 27)
MMOD2 AEPEE FVVEKVLDRRVVNGK.VEYFLKWKGFTDADNTWEPEEN LDCPELIEDF (SEQ ID NO: 28)
DPC PVDLV YAAEKIIQKRVKKGV.VEYRVKWKGWNQRYNTWEPENN ILDRRLIDIY (SEQ ID NO: 29)
MMOD3 VGEQV FAAECILSKRLRKGK.LEYLVKWRGWSSKHNSWEPEEN ILDPRLLLAF (SEQ ID NO: 30)

Figure 14.

```
MOUSE      CHD1      AGA TAT TCT GGA TCT GAT AGT GAT TCA ATC TCG GAA (SEQ ID NO:  31)
CHICKEN    CHD-1A    --- --- --- --- --- --- --- --C --C --- A-A --- (SEQ ID NO:  32)
SPIX       CHD-1A                                 C --C --- --- --- (SEQ ID NO:  33)
CHICKEN    CHD-W     --- --- --- --- --- --- --- --- --C --- --A --- (SEQ ID NO:  34)
SPIX       CHD-W                                  C --C --- --A --- (SEQ ID NO:  35)
HYACINTH   CHD-W                  -- --- --- --- --C --C --- --A --- (SEQ ID NO:  36)
P1                     A TAT TCT GGA TCT GAT AGT GAY TC  (SEQ ID NO:  37)
P3                    AGA TAT TCC GGA TCT GAT AGT GA     (SEQ ID NO:  38)

MOUSE      CHD1      AGG AAA CGG CCG AAG AAA CGT GGG CGA CCC CGC ACT
CHICKEN    CHD-1A    --A --- --- --A --A --G --- --A A-- --T --A --C
SPIX       CHD-1A    --- --- --- --A --A --G --- --A A-- --A --A ---
CHICKEN    CHD-W     --A --- --A --A --A --- --- --A --- --A --A ---
SPIX       CHD-W     --A --- --A --A -GA --- --- --A --- --A --A ---
                                     ^
HYACINTH   CHD-W    --A --- --A --A -GA --- --- --A --- --A --A ---

MOUSE      CHD1      ATC CCT CGG GAG AAT ATT AAA GGA TTT AGT GAT GCG GAG
CHICKEN    CHD-1A    --T --- --A --A --- --- --- --- --- --- --- --A ---
SPIX       CHD-1A    --T --- --A --A --- --A
CHICKEN    CHD-W     --T --C --T --A --C --- --- --- --- --- --- --A ---
SPIX       CHD-W     --T --- --T --A --- ---
P2                                        TTT CCT AAA TCG CTA CGT CT (SEQ ID NO:  39)
HYACINTH   CHD-W     --- --- --- --- --- --- --- --- --- --C --- --A --G
HYACINTH   CHD-W     ATT AGG CGG T
```